AMENDMENTS TO THE CLAIMS

Please cancel without prejudice claims 1-15, 21, 23, 25 and 27. Please amend claims 16 and 18 as set forth below.

1-15. (Cancelled)

16. (Currently Amended) A method of constructing a set of promoter sequences which is suitable for optimizing the expression of a gene in a selected microorganism, said set of promoter sequences covering a range of promoter activities for said gene, the method comprising:

(i) identifying in said microorganism a promoter sequence comprising at least two consensus sequences, which consensus sequences correspond to conserved sequences identified in said microorganism, at least one of the consensus sequences being flanked by a non-conserved nucleotide spacer sequence or both of said consensus sequences being separated by the non-conserved nucleotide spacer sequence, the at least two consensus sequences, when the selected microorganism is

(a) a prokaryotic microorganism, wherein at least one of said at least two consensus sequences is TATAAT and at least one of said at least two consensus sequences is selected from the group consisting of TTGACA and an activator binding site upstream of the TATAAT sequence, or

(b) an eukayotic microorganism, wherein at least one of said at least two consensus sequences is a TATA-box and at least one of said at least two consensus sequences is a UAS upstream of said TATA-box,

(ii) constructing a set of single stranded DNA sequences each of which comprises at least half of each of the consensus sequences, and a non-

conserved nucleotide spacer sequence, at least part of which is varied by a random incorporation of nucleotides selected from the group consisting of the nucleobases A, T, C and G, whilst keeping the at least half of the consensus sequences constant, and

(iii) converting the single stranded DNA sequences into double stranded DNA sequences to obtain the set of promoter sequences covering a range of promoter activities for said gene.

17. (Previously Presented) A method according to claim 16 wherein a plurality of promoter sequences is selected from the set of promoter sequences, said plurality of promoter sequences covering, in said selected microorganisms, a range of promoter activities for said gene, in steps, each step changing the promoter activity by 50-100%.

18. (Currently Amended) A method of controlling in a microorganism the expression of at least one gene product, said method comprising at least one step of changing the expression level of the at least one gene comprising

(i) selecting from a set of promoter sequences a subset of said promoter sequences suitable for optimizing the expression of the at least one gene in a selected microorganism, said subset of the set of promoter sequences covering a range of promoter activities for said gene ~~is~~ in said selected microorganism in small steps each step changing the activity by 50-100%, each promoter sequence of said set of promoter sequences comprising a double stranded DNA sequence, the sense strands of which comprise

at least two consensus sequences, said at least two consensus sequences corresponding to conserved sequences identified in said microorganism, at least half of each of said consensus sequences being kept constant in the set of promoter sequences, the at least two consensus sequences, when the selected microorganism is

a) a prokaryotic microorganism, wherein at least one of said at least two consensus sequences is TATAAT and at least one of said at least two consensus sequences is selected from the group consisting of TTGACA and an activator binding site upstream of the TATAAT sequence, or

b) an eukaryotic ~~microorginism~~ microorganism, wherein at least one of said at least two consensus sequences is ~~TATAAT~~ a TATA-box and at least one of said at least two consensus sequences is ~~selected from the group consisting of TTGACA and an activator binding site upstream of the TATAAT sequence and,~~ a UAS upstream of said TATA-box,

between said consensus sequences or flanking at least one of said consensus sequences, at least one nucleotide spacer sequence, at least part of which, relative to the corresponding spacer sequence of the identified promoter, is varied by random incorporation of nucleotides that are selected from the group consisting of the nulcleobases A, T, C and G,

(ii) transforming said subset of promoter sequences into cells of the organism, placing in each of said cells the gene to be expressed under the control of at least one promoter of the set,

(iii) cultivating the transformed cells to obtain clones thereof and selecting among said clones a clone having, relative to an otherwise identical clone where the at least one gene is under the control of its native promoter, a higher or a lower expression of the at least one gene product.

19. (Cancelled)

20. (Cancelled)

21. (Cancelled)

22. (Previously Presented) An isolated promoter sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:58.

23. (Cancelled)

24. (Cancelled)

25. (Cancelled)

26. (Cancelled)

27. (Cancelled)